



PCT

RAW SEQUENCE LISTING

DATE: 03/08/2005

PATENT APPLICATION: US/10/525,907

TIME: 08:07:17

Input Set : A:\Final Sequence List - 13111-5-US.txt

Output Set: N:\CRF4\03082005\J525907.raw

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3 <110> APPLICANT: Kroger, Burkhard
4     Zelder, Oskar
5     Kolpprogge, Corinna
6     Schroder, Hartwig
7     Hafner, Stefan
9 <120> TITLE OF INVENTION: Method for Production by Fermentation of Sulphur-Containing
Fine
10     Chemicals (metF)
12 <130> FILE REFERENCE: 13111-00005-US
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/525,907
C--> 14 <141> CURRENT FILING DATE: 2005-02-25
14 <150> PRIOR APPLICATION NUMBER: PCT/EP 2003/009451
15 <151> PRIOR FILING DATE: 2003-08-26
17 <150> PRIOR APPLICATION NUMBER: DE 102 39 308.7
18 <151> PRIOR FILING DATE: 2002-08-27
20 <160> NUMBER OF SEQ ID NOS: 77
22 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 984
27 <212> TYPE: DNA
28 <213> ORGANISM: corynebacterium diphtheriae
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(981)
33 <223> OTHER INFORMATION: RDI01260
35 <400> SEQUENCE: 1
36 atg tct gca caa ccg cta cct gct gcg tat cag cgc aca atc acc gat      48
37 Met Ser Ala Gln Pro Leu Pro Ala Ala Tyr Gln Arg Thr Ile Thr Asp
38   1           5           10           15
40 gtc att tcc atg cca aca ccg ggc cag gtt ccg ttt tct gta gag ttt      96
41 Val Ile Ser Met Pro Thr Pro Gly Gln Val Pro Phe Ser Val Glu Phe
42           20           25           30
44 atg ccg cca cga gat gag gca gca gaa gag cga ctc tgg aaa gcc gcc      144
45 Met Pro Pro Arg Asp Glu Ala Ala Glu Glu Arg Leu Trp Lys Ala Ala
46           35           40           45
48 gaa gca ttt cac gac tta gga gcc tct ttt gtc tcc gtt act tat ggt      192
49 Glu Ala Phe His Asp Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly
50   50           55           60
52 gca ggc gga tct agc cgc gag cgc aca atg cgt gtc gcg cac aag ctt      240
53 Ala Gly Gly Ser Ser Arg Glu Arg Thr Met Arg Val Ala His Lys Leu
54   65           70           75           80
56 tct cgt cat ccg ttg acc acg ctc gtt cat ctc acg ctt gtg gaa cac      288
57 Ser Arg His Pro Leu Thr Thr Leu Val His Leu Thr Leu Val Glu His
58           85           90           95

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60 acc caa gaa gaa tta gaa gaa att ctg tgc act tat gcg tcc cac ggg 336
61 Thr Gln Glu Glu Leu Glu Glu Ile Leu Cys Thr Tyr Ala Ser His Gly
62 100 105 110
64 ttg tct aac tta ctt gcc ttg cga ggc gat ccc cct ggc act gac ccg 384
65 Leu Ser Asn Leu Leu Ala Leu Arg Gly Asp Pro Pro Gly Thr Asp Pro
66 115 120 125
68 atg gct ccg tgg gtc cct acc gca ggc ggc cta gat tat gcc aaa gat 432
69 Met Ala Pro Trp Val Pro Thr Ala Gly Gly Leu Asp Tyr Ala Lys Asp
70 130 135 140
72 ttg atc gac ctc gtg cgc aag act gag cag acc tcg cac ttt cag gta 480
73 Leu Ile Asp Leu Val Arg Lys Thr Glu Gln Thr Ser His Phe Gln Val
74 145 150 155 160
76 gga att gct agt ttc cca gaa ggg cac tac cga gcg cct agc att gag 528
77 Gly Ile Ala Ser Phe Pro Glu Gly His Tyr Arg Ala Pro Ser Ile Glu
78 165 170 175
80 gcg gat acg caa ttt aca ttg gaa aag ctg cga gct ggc gca gag ttt 576
81 Ala Asp Thr Gln Phe Thr Leu Glu Lys Leu Arg Ala Gly Ala Glu Phe
82 180 185 190
84 tcg att acc cag atg ttt ttt gat gtc gat cac tat tta cga ctg cga 624
85 Ser Ile Thr Gln Met Phe Phe Asp Val Asp His Tyr Leu Arg Leu Arg
86 195 200 205
88 gat cgc ttg gtt aag gcg gat cct gaa cat gga tca aag ccg atc atc 672
89 Asp Arg Leu Val Lys Ala Asp Pro Glu His Gly Ser Lys Pro Ile Ile
90 210 215 220
92 cca gga ctt atg ccc att acc agc ttg agg tcg gtt cgt agg cag atg 720
93 Pro Gly Leu Met Pro Ile Thr Ser Leu Arg Ser Val Arg Arg Gln Met
94 225 230 235 240
96 gaa tta gca ggt gcc acc ttg cct aag gct tta gaa aaa cgg ctt ctc 768
97 Glu Leu Ala Gly Ala Thr Leu Pro Lys Ala Leu Glu Lys Arg Leu Leu
98 245 250 255
100 gac gca gcg cgc ggc gat gag gaa gct cat cgc ggc gat att cgc aaa 816
101 Asp Ala Ala Arg Gly Asp Glu Glu Ala His Arg Gly Asp Ile Arg Lys
102 260 265 270
104 gta gga atc gaa gtc act act gag atg gca cag cgt ctt att tct gaa 864
105 Val Gly Ile Glu Val Thr Thr Glu Met Ala Gln Arg Leu Ile Ser Glu
106 275 280 285
108 ggg atc cca gac atc cat ttc atg acc atg aat tat gtt cga gcg acc 912
109 Gly Ile Pro Asp Ile His Phe Met Thr Met Asn Tyr Val Arg Ala Thr
110 290 295 300
112 caa gaa gta ctc cat aat ctc ggc atg gcg ccc gcg tgg gga aca cag 960
113 Gln Glu Val Leu His Asn Leu Gly Met Ala Pro Ala Trp Gly Thr Gln
114 305 310 315 320
116 caa ggc cac gac gct att cgc taa 984
117 Gln Gly His Asp Ala Ile Arg
118 325
121 <210> SEQ ID NO: 2
122 <211> LENGTH: 327
123 <212> TYPE: PRT
124 <213> ORGANISM: corynebacterium diptheriae

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126 <400> SEQUENCE: 2

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127 Met Ser Ala Gln Pro Leu Pro Ala Ala Tyr Gln Arg Thr Ile Thr Asp
128 1 5 10 15
130 Val Ile Ser Met Pro Thr Pro Gly Gln Val Pro Phe Ser Val Glu Phe
131 20 25 30
133 Met Pro Pro Arg Asp Glu Ala Ala Glu Glu Arg Leu Trp Lys Ala Ala
134 35 40 45
136 Glu Ala Phe His Asp Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly
137 50 55 60
139 Ala Gly Gly Ser Ser Arg Glu Arg Thr Met Arg Val Ala His Lys Leu
140 65 70 75 80
142 Ser Arg His Pro Leu Thr Thr Leu Val His Leu Thr Leu Val Glu His
143 85 90 95
145 Thr Gln Glu Glu Leu Glu Glu Ile Leu Cys Thr Tyr Ala Ser His Gly
146 100 105 110
148 Leu Ser Asn Leu Leu Ala Leu Arg Gly Asp Pro Pro Gly Thr Asp Pro
149 115 120 125
151 Met Ala Pro Trp Val Pro Thr Ala Gly Gly Leu Asp Tyr Ala Lys Asp
152 130 135 140
154 Leu Ile Asp Leu Val Arg Lys Thr Glu Gln Thr Ser His Phe Gln Val
155 145 150 155 160
157 Gly Ile Ala Ser Phe Pro Glu Gly His Tyr Arg Ala Pro Ser Ile Glu
158 165 170 175
160 Ala Asp Thr Gln Phe Thr Leu Glu Lys Leu Arg Ala Gly Ala Glu Phe
161 180 185 190
163 Ser Ile Thr Gln Met Phe Phe Asp Val Asp His Tyr Leu Arg Leu Arg
164 195 200 205
166 Asp Arg Leu Val Lys Ala Asp Pro Glu His Gly Ser Lys Pro Ile Ile
167 210 215 220
169 Pro Gly Leu Met Pro Ile Thr Ser Leu Arg Ser Val Arg Arg Gln Met
170 225 230 235 240
172 Glu Leu Ala Gly Ala Thr Leu Pro Lys Ala Leu Glu Lys Arg Leu Leu
173 245 250 255
175 Asp Ala Ala Arg Gly Asp Glu Glu Ala His Arg Gly Asp Ile Arg Lys
176 260 265 270
178 Val Gly Ile Glu Val Thr Thr Glu Met Ala Gln Arg Leu Ile Ser Glu
179 275 280 285
181 Gly Ile Pro Asp Ile His Phe Met Thr Met Asn Tyr Val Arg Ala Thr
182 290 295 300
184 Gln Glu Val Leu His Asn Leu Gly Met Ala Pro Ala Trp Gly Thr Gln
185 305 310 315 320
187 Gln Gly His Asp Ala Ile Arg
188 325

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191 <210> SEQ ID NO: 3

192 <211> LENGTH: 924

193 <212> TYPE: DNA

194 <213> ORGANISM: Streptomyces lividans

196 <220> FEATURE:

197 <221> NAME/KEY: CDS

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Input Set : A:\Final Sequence List - 13111-5-US.txt

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198 <222> LOCATION: (1)..(921)
199 <223> OTHER INFORMATION: RSV00084
201 <400> SEQUENCE: 3
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203 Met Ala Leu Gly Thr Ala Ser Thr Arg Thr Asp Arg Ala Arg Thr Val
204 1 5 10 15
206 cgt gac atc ctc gcc acc ggc aag acg acg tac tcg ttc gag ttc tcg 96
207 Arg Asp Ile Leu Ala Thr Gly Lys Thr Thr Tyr Ser Phe Glu Phe Ser
208 20 25 30
210 gcg ccg aag acg ccc aag ggc gag aag aac ctc tgg agc gcg ctg cgg 144
211 Ala Pro Lys Thr Pro Lys Gly Glu Lys Asn Leu Trp Ser Ala Leu Arg
212 35 40 45
214 cgg gtc gag gcc gtg gcc ccg gac ttc gtc tcc gtg acc tac ggc gcc 192
215 Arg Val Glu Ala Val Ala Pro Asp Phe Val Ser Val Thr Tyr Gly Ala
216 50 55 60
218 ggc ggc tcc acg cgc gcc ggc acg gtc cgc gag acc cag cag atc gtc 240
219 Gly Gly Ser Thr Arg Ala Gly Thr Val Arg Glu Thr Gln Gln Ile Val
220 65 70 75 80
222 gcc gac acc acg ctg acc ccg gtg gcc cac ctc acc gcc gtc gac cac 288
223 Ala Asp Thr Thr Leu Thr Pro Val Ala His Leu Thr Ala Val Asp His
224 85 90 95
226 tcc gtc gcc gag ctg cgc aac atc atc ggc cag tac gcc gac gcc ggg 336
227 Ser Val Ala Glu Leu Arg Asn Ile Ile Gly Gln Tyr Ala Asp Ala Gly
228 100 105 110
230 atc cgc aac atg ctg gcc gtg cgc ggc gac ccg ccc ggc gac ccg aac 384
231 Ile Arg Asn Met Leu Ala Val Arg Gly Asp Pro Pro Gly Asp Pro Asn
232 115 120 125
234 gcc gac tgg atc gcg cac ccc gag ggc ctg acc tac gcg gcc gaa ctg 432
235 Ala Asp Trp Ile Ala His Pro Glu Gly Leu Thr Tyr Ala Ala Glu Leu
236 130 135 140
238 gtc agg ctc atc aag gag tcg gga gac ttc tgc gtc ggc gtc gcc gcc 480
239 Val Arg Leu Ile Lys Glu Ser Gly Asp Phe Cys Val Gly Val Ala Ala
240 145 150 155 160
242 ttc ccc gag atg cac ccg cgc tcc gcc gac tgg gac acg gac gtc acg 528
243 Phe Pro Glu Met His Pro Arg Ser Ala Asp Trp Asp Thr Asp Val Thr
244 165 170 175
246 aac ttc gtc gac aag tgc cgg gcc ggc gcc gac tac gcc atc acc cag 576
247 Asn Phe Val Asp Lys Cys Arg Ala Gly Ala Asp Tyr Ala Ile Thr Gln
248 180 185 190
250 atg ttc ttc cag ccc gac tcc tac ctc cgg ctg cgc gac cgg gtc gcc 624
251 Met Phe Phe Gln Pro Asp Ser Tyr Leu Arg Leu Arg Asp Arg Val Ala
252 195 200 205
254 gcg gcc ggc tgc gcg acc ccg gtc att ccc gag gtc atg ccg gtg acc 672
255 Ala Ala Gly Cys Ala Thr Pro Val Ile Pro Glu Val Met Pro Val Thr
256 210 215 220
258 agt gtg aag atg ctg gag agg ttg ccg aag ctc agc aac gcc tcg ttc 720
259 Ser Val Lys Met Leu Glu Arg Leu Pro Lys Leu Ser Asn Ala Ser Phe
260 225 230 235 240
262 ccg gcg gag ctg aaa gag cgg atc ctc aca gcc aag gac gat ccg gcg 768

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VERIFICATION SUMMARY

DATE: 03/08/2005

PATENT APPLICATION: US/10/525,907

TIME: 08:07:18

Input Set : A:\Final Sequence List - 13111-5-US.txt

Output Set: N:\CRF4\03082005\J525907.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

RAW SEQUENCE LISTING

DATE: 03/08/2005

PATENT APPLICATION: US/10/525,907

TIME: 08:07:17

Input Set : A:\Final Sequence List - 13111-5-US.txt

Output Set: N:\CRF4\03082005\J525907.raw

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263 Pro Ala Glu Leu Lys Glu Arg Ile Leu Thr Ala Lys Asp Asp Pro Ala
264          245          250          255
266 gct gta cgc tcg atc ggc atc gag ttc gcc acg gag ttc tgc gcg cgg 816
267 Ala Val Arg Ser Ile Gly Ile Glu Phe Ala Thr Glu Phe Cys Ala Arg
268          260          265          270
270 ctg ctg gcc gag gga gtg cca gga ctg cac ttc atc acg ctc aac aac 864
271 Leu Leu Ala Glu Gly Val Pro Gly Leu His Phe Ile Thr Leu Asn Asn
272          275          280          285
274 tcc acg gcg acg ctg gaa atc tac gag aac ctg ggc ctg cac cac cca 912
275 Ser Thr Ala Thr Leu Glu Ile Tyr Glu Asn Leu Gly Leu His His Pro
276          290          295          300
278 ccg cgg gcc tag 924
279 Pro Arg Ala
280 305
283 <210> SEQ ID NO: 4
284 <211> LENGTH: 307
285 <212> TYPE: PRT
286 <213> ORGANISM: Streptomyces lividans
288 <400> SEQUENCE: 4
289 Met Ala Leu Gly Thr Ala Ser Thr Arg Thr Asp Arg Ala Arg Thr Val
290 1 5 10 15
292 Arg Asp Ile Leu Ala Thr Gly Lys Thr Tyr Ser Phe Glu Phe Ser
293 20 25 30
295 Ala Pro Lys Thr Pro Lys Gly Glu Lys Asn Leu Trp Ser Ala Leu Arg
296 35 40 45
298 Arg Val Glu Ala Val Ala Pro Asp Phe Val Ser Val Thr Tyr Gly Ala
299 50 55 60
301 Gly Gly Ser Thr Arg Ala Gly Thr Val Arg Glu Thr Gln Gln Ile Val
302 65 70 75 80
304 Ala Asp Thr Thr Leu Thr Pro Val Ala His Leu Thr Ala Val Asp His
305 85 90 95
307 Ser Val Ala Glu Leu Arg Asn Ile Ile Gly Gln Tyr Ala Asp Ala Gly
308 100 105 110
310 Ile Arg Asn Met Leu Ala Val Arg Gly Asp Pro Pro Gly Asp Pro Asn
311 115 120 125
313 Ala Asp Trp Ile Ala His Pro Glu Gly Leu Thr Tyr Ala Ala Glu Leu
314 130 135 140
316 Val Arg Leu Ile Lys Glu Ser Gly Asp Phe Cys Val Gly Val Ala Ala
317 145 150 155 160
319 Phe Pro Glu Met His Pro Arg Ser Ala Asp Trp Asp Thr Asp Val Thr
320 165 170 175
322 Asn Phe Val Asp Lys Cys Arg Ala Gly Ala Asp Tyr Ala Ile Thr Gln
323 180 185 190
325 Met Phe Phe Gln Pro Asp Ser Tyr Leu Arg Leu Arg Asp Arg Val Ala
326 195 200 205
328 Ala Ala Gly Cys Ala Thr Pro Val Ile Pro Glu Val Met Pro Val Thr
329 210 215 220
331 Ser Val Lys Met Leu Glu Arg Leu Pro Lys Leu Ser Asn Ala Ser Phe
332 225 230 235 240

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